



SEQUENCE LISTING

<110> Hoogenboom, Hendricus R.J.M.
Henderikx, Maria P.G.

<120> MUCIN-1 SPECIFIC BINDING MEMBERS AND
METHODS OF USE THEREOF

<130> 10280-075002

<140> US 09/822,698

<141> 2001-03-30

<150> US 09/538,913

<151> 2000-03-30

<160> 116

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain variable region of the MUC1- specific
binding domain of PH1 Fab antibody

<400> 1

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ile | Val | Leu | Thr | Gln | Ser | Pro | Leu | Ser | Leu | Pro | Val | Thr | Pro | Gly |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Glu | Pro | Ala | Ser | Ile | Ser | Cys | Arg | Ser | Ser | Gln | Ser | Leu | Leu | His | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Asn | Gly | Tyr | Thr | Tyr | Leu | Asp | Trp | Tyr | Leu | Gln | Lys | Pro | Gly | Gln | Ser |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Pro | Gln | Leu | Leu | Ile | Tyr | Ser | Gly | Ser | His | Arg | Ala | Ser | Gly | Val | Pro |
| | | | 50 | | | 55 | | | | 60 | | | | | |
| Asp | Arg | Phe | Ser | Gly | Ser | Val | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Arg | Ile |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Ser | Arg | Val | Glu | Ala | Glu | Asp | Val | Gly | Val | Tyr | Tyr | Cys | Met | Gln | Gly |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Leu | Gln | Ser | Pro | Phe | Thr | Phe | Gly | Pro | Gly | Thr | Lys | Val | Asp | Ile | Lys |
| | | | 100 | | | | | 105 | | | | | | 110 | |
| Arg | | | | | | | | | | | | | | | |

<210> 2

<211> 339

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding of light chain variable
region of the MUC1- specific binding domain of PH1
Fab antibody

<400> 2
 gaaattgtgc tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc 60
 atctcctgca ggtctagtc gagcctcctg catagtaatg gatacaccta tttggattgg 120
 tacctgcaga agccagggca gtctccacag ctctgatct attcgggttc tcatcgggcc 180
 tccgggggtcc ctgacaggtt cagtggcagt gtatcaggca cagattttac actgagaatc 240
 agcagagtgg aggctgagga tgttggagtt tattactgca tgcaggggtct acagagtcca 300
 ttcacttttcg gccctgggac caaagtggat atcaaacga 339

<210> 3
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain variable region of the MUC1- specific
 binding domain of PH1 Fab antibody

<400> 3
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Asn
 20 25 30
 Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 4
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence coding of heavy chain variable
 region of the MUC1- specific binding domain of PH1
 Fab antibody

<400> 4
 caggtccagc tgggtgcagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt cagctttaga agtaacgcca tgggctgggt ccgccaggct 120
 ccaggggaagg ggtctgagtg ggtctcaggt attagtggta gtggtggcag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaataa acagcctgag agccgaggac acggccgtat attattgtgc gaaacatacc 300
 gggggggggcg tttgggaccc cattgactac tggggccagg gaaccctgggt caccgtctca 360
 agc 363

<210> 5
 <211> 381

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> MUC1-specific immunocytokine bivPH1-IL-2

<400> 5

| | | | | | | | | | | | | | | | |
|----------|-----|-----|-----|----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|
| Gln 1 | Val | Gln | Leu | Val 5 | Gln | Ser | Gly | Gly | Gly 10 | Leu | Val | Gln | Pro | Gly 15 | Gly |
| Ser | Leu | Arg | Leu | Ser | Cys | Ala | Ala | Ser | Gly | Phe | Thr | Phe | Arg | Ser | Asn |
| | | | 20 | | | | | 25 | | | | 30 | | | |
| Ala | Met | Gly | Trp | Val | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Val |
| | | 35 | | | | 40 | | | | | 45 | | | | |
| Ser | Gly | Ile | Ser | Gly | Ser | Gly | Gly | Ser | Thr | Tyr | Tyr | Ala | Asp | Ser | Val |
| | 50 | | | | 55 | | | | | 60 | | | | | |
| Lys | Gly | Arg | Phe | Thr | Ile | Ser | Arg | Asp | Asn | Ser | Lys | Asn | Thr | Leu | Tyr |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Leu | Gln | Met | Asn | Ser | Leu | Arg | Ala | Glu | Asp | Thr | Ala | Val | Tyr | Tyr | Cys |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Ala | Lys | His | Thr | Gly | Gly | Gly | Val | Trp | Asp | Pro | Ile | Asp | Tyr | Trp | Gly |
| | | | 100 | | | | 105 | | | | 110 | | | | |
| Gln | Gly | Thr | Leu | Val | Thr | Val | Ser | Ser | Gly | Gly | Gly | Ala | Leu | Glu | Ile |
| | | 115 | | | | 120 | | | | | 125 | | | | |
| Val | Leu | Thr | Gln | Ser | Pro | Leu | Ser | Leu | Pro | Val | Thr | Pro | Gly | Glu | Pro |
| | 130 | | | | 135 | | | | | 140 | | | | | |
| Ala | Ser | Ile | Ser | Cys | Arg | Ser | Ser | Gln | Ser | Leu | Leu | His | Ser | Asn | Gly |
| 145 | | | | 150 | | | | 155 | | | | | | 160 | |
| Tyr | Thr | Tyr | Leu | Asp | Trp | Tyr | Leu | Gln | Lys | Pro | Gly | Gln | Ser | Pro | Gln |
| | | | 165 | | | | | 170 | | | | 175 | | | |
| Leu | Leu | Ile | Tyr | Ser | Gly | Ser | His | Arg | Ala | Ser | Gly | Val | Pro | Asp | Arg |
| | | 180 | | | | 185 | | | | | 190 | | | | |
| Phe | Ser | Gly | Ser | Val | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Arg | Ile | Ser | Arg |
| | | 195 | | | | 200 | | | | | 205 | | | | |
| Val | Glu | Ala | Glu | Asp | Val | Gly | Val | Tyr | Tyr | Cys | Met | Gln | Gly | Leu | Gln |
| | 210 | | | | 215 | | | | | 220 | | | | | |
| Ser | Pro | Phe | Thr | Phe | Gly | Pro | Gly | Thr | Lys | Val | Asp | Ile | Lys | Arg | Gly |
| 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| Gly | Gly | Ser | Gly | Gly | Gly | Ala | Leu | Ala | Pro | Thr | Ser | Ser | Ser | Thr | Lys |
| | | | 245 | | | | | 250 | | | | | 255 | | |
| Lys | Thr | Gln | Leu | Gln | Leu | Glu | His | Leu | Leu | Leu | Asp | Leu | Gln | Met | Ile |
| | | 260 | | | | | 265 | | | | | 270 | | | |
| Leu | Asn | Gly | Ile | Asn | Asn | Tyr | Lys | Asn | Pro | Lys | Leu | Thr | Arg | Met | Leu |
| | | 275 | | | | 280 | | | | | 285 | | | | |
| Thr | Phe | Lys | Phe | Tyr | Met | Pro | Lys | Lys | Ala | Thr | Glu | Leu | Lys | His | Leu |
| | 290 | | | | 295 | | | | 300 | | | | | | |
| Gln | Cys | Leu | Glu | Glu | Glu | Leu | Lys | Pro | Leu | Glu | Glu | Val | Leu | Asn | Leu |
| 305 | | | | 310 | | | | 315 | | | | | | 320 | |
| Ala | Gln | Ser | Lys | Asn | Phe | His | Leu | Arg | Pro | Arg | Asp | Leu | Ile | Ser | Asn |
| | | | 325 | | | | | 330 | | | | 335 | | | |
| Ile | Asn | Val | Ile | Val | Leu | Glu | Leu | Lys | Gly | Ser | Glu | Thr | Thr | Phe | Met |
| | | 340 | | | | | 345 | | | | 350 | | | | |
| Cys | Glu | Tyr | Ala | Asp | Glu | Thr | Ala | Thr | Ile | Val | Glu | Phe | Leu | Asn | Arg |
| | | | | | | | | | | | | | | | |

<210> 6

<211> 1143
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MUC1-specific immunocytokine bivPH1-IL-2

<400> 6
 caggtccagc tgggtgcagtc tggggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt cacgtttaga agtaacgcc a tgggctgggt ccgccagget 120
 ccagggaagg ggctggagtg ggtctcaggt attagtggta gtggtggcag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag agccgaggac acggccgtat attattgtgc gaaacatacc 300
 gggggggggcg tttgggaccc cattgactac tggggccagg gaaccctggg caccgtctca 360
 agcggaggcg gtgcacttga aattgtgctg actcagtcct cactctccct gcccgtcacc 420
 cctggagagc cggcctccat ctctgcagg tctagtcaga gcctcctgca tagtaatgga 480
 tacacctatt tggattggta cctgcagaag ccagggcagt ctccacagct cctgatctat 540
 tcgggttctc atcgggcctc cgggggtccct gacagggttc gtggcagtg atcaggcaca 600
 gatttttacac tgagaatcag cagagtggag gctgaggatg ttggagttaa ttactgcatg 660
 cagggtctac agagtccatt cactttcggc cctgggacca aagtggatat caaacgaggg 720
 ggtggatcag gcggcggggc ctagcacct acttcaagtt ctacaaagaa aacacagcta 780
 caactggagc atttactgct ggatttacag atgattttga atggaattaa taattacaag 840
 aatcccaaac tcaccaggat gctcacattt aagttttaca tgcccaagaa ggccacagaa 900
 ctgaaacatc ttcagtgtct agaagaagaa ctcaaacctc tggaggaagt gctaaattta 960
 gctcaaagca aaaactttca cttaagaccc agggacttaa tcagcaatat caacgtaata 1020
 gttctggaac taaagggatc tgaaacaaca ttcattgtgtg aatatgctga tgagacagca 1080
 accattgtag aattttctgaa cagatggatt accttttgtc aaagcatcat ctcaacactg 1140
 act 1143

<210> 7
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> peptide of MUC1 protein

<400> 7
 Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly
 1 5 10 15
 Ser Thr Ala Pro
 20

<210> 8
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> peptide of MUC1 protein

<400> 8
 Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro
 1 5 10 15
 Pro Ala His Gly
 20

<210> 9
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> CH1FOR primer

 <400> 9
 gtccttgacc aggcagccca gggc 24

 <210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> pUC-reverse primer

 <400> 10
 agcggataac aatttcacac agg 23

 <210> 11
 <211> 44
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> VL backward primer

 <400> 11
 accgcctcca ccagtgact tgaaattgtg ctgactcagt ctcc 44

 <210> 12
 <211> 51
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> VL forward primer

 <400> 12
 accgcctcca ccgggcgcgc cttattaaca ctctcccctg ttgaagctct t 51

 <210> 13
 <211> 61
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> VL backward primer for light chain variable region
 of the PH1 Fab antibody with additional linker and
 restriction sites

 <400> 13
 gccgatcgct ctggtcaccg tctcaagcgg aggcggtgca cttgaaattg tgctgactca 60
 g 61

<210> 14
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VL forward primer for light chain variable region
 of the PH1 Fab antibody with additional linker and
 restriction sites

<400> 14
 gtctcgcgag cggccgccga ttggatatcc actttgttcc cagggccgaa 50

<210> 15
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence coding for a nine amino acid
 linker

<400> 15
 gggggtggat caggcggcgg ggcccta 27

<210> 16
 <211> 69
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PH1-IL-2 backward primer

<400> 16
 accaaagtgg atatcaaacg aggggggtgga tcaggcggcg gggccctagc acctacttca 60
 agttctaca 69

<210> 17
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PH1-IL-2 forward primer

<400> 17
 gtcccgcgtg cggccgcagt cagtgttgag atgatgcttt gacaaaagg 49

<210> 18
 <211> 98
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain variable region from a DP47 germ line

[illegible]

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<210> 19
<211> 100
<212> PRT
<213> Artificial Sequence
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<220>
<223> light chain variable region from a DP47 germ line

[illegible]

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<210> 20
<211> 14
<212> PRT
<213> Artificial Sequence
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<220>
<223> myc tag peptide
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<400> 20
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
1 5 10

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<210> 21
<211> 42
<212> DNA
<213> Artificial Sequence
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<220>

<223> nucleotide sequence coding of myc tag peptide

<400> 21

gaacaaaaac tcatctcaga agaggatctg aatggggccg ca

42

<210> 22

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> hexahistidine peptide

<400> 22

His His His His His His

1

5

<210> 23

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding of hexahistidine peptide

<400> 23

catcaccatc atcaccat

18

<210> 24

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> immunoglobulin kappa light chain of MUC1-specific PH1-IgG1

<400> 24

Glu Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly

1

5

10

15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser

20

25

30

Asn Gly Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35

40

45

Pro Gln Leu Leu Ile Tyr Ser Gly Ser His Arg Ala Ser Gly Val Pro

50

55

60

Asp Arg Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Arg Ile

65

70

75

80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly

85

90

95

Leu Gln Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys

100

105

110

Arg Gly Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp

115

120

125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn

| | | | | |
|---|-----|-----|-----|-----|
| 130 | | 135 | | 140 |
| Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu | | | | |
| 145 | | 150 | | 155 |
| Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp | | | | |
| | 165 | | 170 | 175 |
| Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr | | | | |
| | 180 | | 185 | 190 |
| Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser | | | | |
| | 195 | | 200 | 205 |
| Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys | | | | |
| 210 | | 215 | | 220 |

<210> 25

<211> 663

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding of immunoglobulin kappa
light chain of MUC1-specific PH1-IgG1

<400> 25

| | | | | | | |
|-------------|-------------|------------|------------|------------|------------|-----|
| gaaattgtgc | tgactcagtc | tccactctcc | ctgcccgtca | cccctggaga | gccggcctcc | 60 |
| atctcctgca | ggctctagtca | gagcctcctg | catagtaatg | gatacaccta | tttggattgg | 120 |
| tacctgcaga | agccagggca | gtctccacag | ctcctgatct | attcgggttc | tcatcggggc | 180 |
| tccgggggtcc | ctgacagggtt | cagtggcagt | gtatcaggca | cagattttac | actgagaatc | 240 |
| agcagagtgg | aggctgagga | tgttggagtt | tattactgca | tgcagggtct | acagagtcca | 300 |
| ttcacttttcg | gccctgggac | caaagtggat | atcaaacgag | gaactgtggc | tgcaccatct | 360 |
| gtcttcatct | tcccgccatc | tgatgagcag | ttgaaatctg | gaactgcctc | tgttgtgtgc | 420 |
| ctgctgaata | acttctatcc | cagagaggcc | aaagtacagt | ggaagggtga | taacgccctc | 480 |
| caatcgggta | actcccagga | gagtgtcaca | gagcaggaca | gcaaggacag | cacctacagc | 540 |
| ctcagcagca | ccctgacgct | gagcaaagca | gactacgaga | aacacaaagt | ctacgcctgc | 600 |
| gaagtcaccc | atcagggcct | gagttcaccg | gtgacaaaga | gcttcaacag | gggagagtgt | 660 |
| tag | | | | | | 663 |

<210> 26

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> immunoglobulin heavy chain of MUC1-specific
PH1-IgG1

<400> 26

| | |
|---|----|
| Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly | |
| 1 | 15 |
| Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Asn | |
| 20 | 30 |
| Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val | |
| 35 | 45 |
| Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val | |
| 50 | 60 |
| Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr | |
| 65 | 80 |
| Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys | |
| 85 | 95 |

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 210 215 220
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 225 230 235 240
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 325 330 335
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 355 360 365
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 Pro Gly Lys
 450

<210> 27

<211> 1356

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding of immunoglobulin heavy
chain of MUC1-specific PH1-IgG1

<400> 27

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cagggtccagc tgggtgcagtc tggggggaggc ttggtacagc ctgggggggtc cctgagactc      60
tcctgtgcag cctctggatt cacgtttaga agtaacgcca tgggctgggt ccgccaggct      120
ccaggggaagg ggctggagtg ggtctcagggt attagtggta gtggtggcag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcaaataga acagcctgag agccgaggac acggccgtat attattgtgc gaaacataacc      300
ggggggggcg tttgggaccc cattgactac tggggccagg gaaccctggg caccgtctca      360
agcgccctcca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct      420
ggggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg      480
tcgtggaact caggcgccct gaccagcggc gtccacacct tcccggctgt cctacagtcc      540
tcaggactct actccctcag cagcgtagtg accgtgccct ccagcagctt gggcacccag      600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag      660
cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg      720
ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca cctcatgat ctcccggacc      780
cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgagggt caagttcaac      840
tgggtacgtg acggcgtgga ggtgcataat gccaaagacaa agccgcggga ggagcagtac      900
aacagcacgt accgtgtggg cagcgtcctc accgtcctgc accaggactg gctgaatggc      960
aaggagtaca agtgcaagggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc     1020
tccaaagcca aagggcagcc ccgagaacca cagggtgtaca ccctgcccc atcccgggat     1080
gagctgacca agaaccagggt cagcctgacc tgctgtgtca aaggcttcta tcccagcgac     1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc     1200
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg     1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac     1320
acgcagaaga gcctctcctt aagtccggga aaataa                                1356

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<210> 28

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> MUC1-specific binding member

<221> VARIANT

<222> 1

<223> Xaa = Ala, Ser, Thr, or Val

<221> VARIANT

<222> 2

<223> Xaa = Lys, Ile Arg, or Gln

<221> VARIANT

<222> 3

<223> Xaa = Gly, Arg, Val, Glu, Ser, or Ala

<221> CONFLICT

<222> 4

<223> Xaa = Asp or Asn

<221> VARIANT

<222> 5

<223> Xaa = Ile, Leu, Met, Phe, or Val

<221> VARIANT

<222> (6)...(0)

<223> Xaa = Asp, Gly, Lys, Asn, Ala, His, Arg, Ser, Val,
or Tyr

<221> VARIANT
 <222> (7)...(0)
 <223> Xaa = Tyr, His, Lys, Asn, Asp, Ser, or Pro

 <400> 28
 Xaa Xaa His Thr Gly Xaa Gly Val Trp Xaa Pro Xaa Xaa Xaa
 1 5 10

 <210> 29
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> region of a MUC1-specific binding member

 <400> 29
 Ala Lys His Thr Gly Arg Gly Val Trp Asp Pro Ile Gly Tyr
 1 5 10

 <210> 30
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> region of a MUC1-specific binding member

 <400> 30
 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Lys His
 1 5 10

 <210> 31
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> region of a MUC1-specific binding member

 <400> 31
 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr
 1 5 10

 <210> 32
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> region of a MUC1-specific binding member

 <400> 32
 Ala Ile His Thr Gly Gly Gly Val Trp Asp Pro Ile Lys Tyr
 1 5 10

 <210> 33

<211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<221> misc_feature
 <222> 16, 17, 18
 <223> n may be varied according to the disclosure to
 form mutagenic primer

<400> 33
 ggattcacgt ttagannnaa cgccatgggc tgg

33

<210> 34
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<221> misc_feature
 <222> 16, 17, 18 22, 23, 24
 <223> n may be varied according to the disclosure to
 form mutagenic primer sequences

<400> 34
 cacggagtct gcgtannntg tnnngccacc actaccact

39

<210> 35
 <211> 90
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<221> misc_feature
 <222> 34-75
 <223> n may be varied according to the disclosure to
 form mutagenic primer sequences

<400> 35
 ctatgagacg gtgaccaggg ttccctggcc ccannnnnnnn nnnnnnnnnnn nnnnnnnnnnn
 nnnnnnnnnnn nnnnnacaat aatatacggc

60

90

<210> 36
 <211> 90
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<221> misc_feature

<222> 56, 57, 59, 60, 62, 63, 65, 66, 68, 69

<223> n may be varied according to the disclosure to
form mutagenic primer sequences

<400> 36

ctatgagacg gtgaccaggg ttccctggcc ccagtagtca atgggggtccc aaacmnnmnn 60
mnnmnnmnnnt ttcgcacaat aatatacggc 90

<210> 37

<211> 90

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<221> misc_feature

<222> 41, 42, 44, 45, 47, 48, 50, 51, 53, 54

<223> n may be varied according to the disclosure to
form mutagenic primer sequences

<400> 37

ctatgagacg gtgaccaggg ttccctggcc ccagtagtcm nnnnnnnnnnn nmnnngccccc 60
cccgtatgt ttcgcacaat aatatacggc 90

<210> 38

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> HuJH4-5-FOR primer

<400> 38

tgaggagacg gtgaccaggg ttcc 24

<210> 39

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> VH1c back Sfi primer

<400> 39

gtcctcgcaa ctgcggccca gccggccatg gccsaggtcc agctggtrca gtctgg 56

<210> 40

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> PAP peptide epitope of MUC1 bound by PH1 Fab
antibody

<400> 40

Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala Leu
 1 5 10 15

<210> 41
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain
 variable region

<400> 41
 Ala Lys His Asn Thr Ser Lys Val Trp Asp Pro Ile Asp Tyr Trp Gly
 1 5 10 15

<210> 42
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3
 region

<400> 42
 gcgaaacata atacgtctaa ggtttgggac cccattgact actggggc

48

<210> 43
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain
 variable region

<400> 43
 Ala Lys Ser Ser Thr Thr Thr Val Trp Asp Pro Ile Asp Tyr Trp Gly
 1 5 10 15

<210> 44
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3
 region

<400> 44
 gcgaaatcta gtactacgac ggtttgggac cccattgact actggggc

48

<210> 45
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>

<223> a mutant CDR3 region

<221> VARIANT

<222> 3

<223> Xaa indicates end of amino acid sequence because
mutation in nucleotide sequence forms a
translational stop codon

<400> 45

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Lys | Xaa | Pro | Met | Ala | Asn | Val | Trp | Asp | Pro | Ile | Asp | Tyr | Trp | Gly |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

<210> 46

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3
region

<400> 46

gcgaaatagc ctatggcgaa tgtttgggac cccattgact actggggc

48

<210> 47

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region

<221> VARIANT

<222> 3

<223> Xaa indicates end of amino acid sequence because
mutation in nucleotide sequence forms a
translational stop codon

<400> 47

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Lys | Xaa | His | Thr | Lys | Thr | Val | Trp | Asp | Pro | Ile | Asp | Tyr | Trp | Gly |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

<210> 48

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3
region

<400> 48

gcgaaatagc atacgaagac ggtttgggac cccattgact actggggc

48

<210> 49

<211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain
 variable region

<400> 49
 Ala Lys Ile Thr Val Ser Arg Val Trp Asp Pro Ile Asp Tyr Trp Gly
 1 5 10 15

<210> 50
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3
 region

<400> 50
 gcgaaaatta ctgttagtcg tgtttgggac cccattgact actggggc 48

<210> 51
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain
 variable region

<400> 51
 Ala Lys Arg Tyr Leu Tyr Asp Val Trp Asp Pro Ile Asp Tyr Trp Gly
 1 5 10 15

<210> 52
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3
 region

<400> 52
 gcgaaacgtt atctgtatga tgtttgggac cccattgact actggggc 48

<210> 53
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain
 variable region

<400> 53

Ala Lys His Thr Gly Gly Gly Thr Leu Gln Arg Leu Asp Tyr Trp Gly
1 5 10 15

<210> 54

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3
region

<400> 54

gcgaaacata ccggggggggg cactttgcag cggttgact actggggc

48

<210> 55

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain
variable region

<400> 55

Ala Lys His Thr Gly Gly Gly Thr Gln Thr Pro Cys Asp Tyr Trp Gly
1 5 10 15

<210> 56

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3
region

<400> 56

gcgaaacata ccggggggggg cactcagact ccgtgtgact actggggc

48

<210> 57

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain
variable region

<400> 57

Ala Lys His Thr Gly Gly Gly Arg Arg Ile Cys His Asp Tyr Trp Gly
1 5 10 15

<210> 58

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3 region

<400> 58

gcgaaacata ccgggggggg ccgtcgtatt tgatcatgact actgggggc

48

<210> 59

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region

<221> VARIANT

<222> 8, 10, 11

<223> Xaa indicates end of amino acid sequence because mutation in nucleotide sequence forms a translational stop codon

<400> 59

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Lys | His | Thr | Gly | Gly | Gly | Xaa | Arg | Xaa | Xaa | Arg | Asp | Tyr | Trp | Gly |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

<210> 60

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3 region

<400> 60

gcgaaacata ccgggggggg ctagcggttag tagcgggact actgggggc

48

<210> 61

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain variable region

<400> 61

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Lys | His | Thr | Gly | Gly | Gly | Gln | Lys | Leu | Gln | Leu | Asp | Tyr | Trp | Gly |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

<210> 62

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3
region

<400> 62

gcgaaacata ccggggggggg ccagaagctg cagctggact actgggggc

48

<210> 63

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region

<221> VARIANT

<222> 2

<223> Xaa indicates end of amino acid sequence because
mutation in nucleotide sequence forms a
translational stop codon; or when designated as
"s" in the disclosure, Xaa is serine

<400> 63

Ala Xaa His Thr Gly Gly Arg Gly Trp Asp Pro Ile Asp Tyr Trp Gly
1 5 10 15

<210> 64

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3
region

<400> 64

gcgtsacata cggggggggcg cggttgggac cccattgact actgggggc

48

<210> 65

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 65

Ala Asn Gln Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly
1 5 10 15

<210> 66

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3
region

<400> 66

gcgaaccaga ctggggggggg cgtttggggac cccattgact actgggggc

48

<210> 67

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 67

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Arg | His | Thr | Gly | Gly | Gly | Val | Trp | Asp | Pro | Ile | Tyr | Tyr | Trp | Gly |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

<210> 68

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3
region

<400> 68

gcgagacata ccggtggggg cgtktgggat cccatatact actgggggc

48

<210> 69

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 69

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Lys | Pro | Thr | Gly | Gly | Gly | Ala | Trp | Asp | Pro | Ile | Asp | Tyr | Trp | Gly |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

<210> 70

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence coding for a mutant CDR3
region

<400> 70

gcgaaacctt ccggggggggg cgcttggggac cccattgact actgggggc

48

<210> 71
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mutant CDR3 region of an antibody heavychain
 variable region

<400> 71
 Ala Lys His Thr Gly Val Gly Val Trp His Pro Ile Tyr Tyr Trp Gly
 1 5 10 15

<210> 72
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3
 region

<400> 72
 gcgaaacata ccggggtggg cgtttggcac cccatctact actgggggc

48

<210> 73
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mutant CDR3 region of an antibody heavychain
 variable region

<400> 73
 Ala Lys His Thr Gly Val Gly Val Trp Asp Pro Ile Lys Tyr
 1 5 10

<210> 74
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mutant CDR3 region of an antibody heavychain
 variable region

<400> 74
 Ala Lys His Thr Gly Glu Gly Val Trp Asp Pro Ile Lys Tyr
 1 5 10

<210> 75
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 75

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Lys
1 5 10

<210> 76

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 76

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr
1 5 10

<210> 77

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 77

Ala Arg His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr
1 5 10

<210> 78

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 78

Ser Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr
1 5 10

<210> 79

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 79

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly His

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<220>
<223> mutant CDR3 region of an antibody heavychain
      variable region
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<220>
<223> mutant CDR3 region of an antibody heavychain
      variable region
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<223> mutant CDR3 region of an antibody heavychain
      variable region
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<220>
<223> mutant CDR3 region of an antibody heavychain
      variable region
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<210> 84
<211> 14
<212> PRT
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<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 84

Ala Arg His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Tyr
1 5 10

<210> 85

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 85

Ala Lys His Thr Gly Ser Gly Val Trp Asp Pro Ile Asn Tyr
1 5 10

<210> 86

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 86

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Asp
1 5 10

<210> 87

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 87

Ala Lys His Thr Gly Val Gly Val Trp Asp Pro Met Asn Tyr
1 5 10

<210> 88

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 88

Thr Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Tyr
1 5 10

<210> 89

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 89

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ala Tyr
1 5 10

<210> 90

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 90

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ala Asn
1 5 10

<210> 91

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 91

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Phe Ala Tyr
1 5 10

<210> 92

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 92

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Met Ala Ser
1 5 10

<210> 93
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mutant CDR3 region of an antibody heavychain
 variable region

<400> 93
 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Met Asp Tyr
 1 5 10

<210> 94
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mutant CDR3 region of an antibody heavychain
 variable region

<400> 94
 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile His Tyr
 1 5 10

<210> 95
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mutant CDR3 region of an antibody heavychain
 variable region

<400> 95
 Ala Ile His Thr Gly Ala Gly Val Trp Asp Pro Ile Arg Tyr
 1 5 10

<210> 96
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mutant CDR3 region of an antibody heavychain
 variable region

<400> 96
 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ser Ser
 1 5 10

<210> 97
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 97

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Asp
1 5 10

<210> 98

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 98

Val Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Val Tyr
1 5 10

<210> 99

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 99

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Val Asp Tyr
1 5 10

<210> 100

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 100

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Val Pro
1 5 10

<210> 101

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
variable region

<400> 101

Val Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ala Tyr
 1 5 10

<210> 102

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
 variable region

<400> 102

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile His Asn
 1 5 10

<210> 103

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
 variable region

<400> 103

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Met His Tyr
 1 5 10

<210> 104

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
 variable region

<400> 104

Ala Lys His Thr Gly Gly Gly Val Trp Asn Pro Ile Asp Tyr
 1 5 10

<210> 105

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> mutant CDR3 region of an antibody heavychain
 variable region

<400> 105

Val Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr
 1 5 10

<210> 106

<211> 14

<212> PRT
 <213> Artificial Sequence

 <220>
 <223> mutant CDR3 region of an antibody heavychain
 variable region

 <400> 106
 Ala Lys His Thr Gly Ala Gly Val Trp Asp Pro Ile Asp Tyr
 1 5 10

 <210> 107
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> mutant CDR3 region of an antibody heavychain
 variable region

 <400> 107
 Ala Gln His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr
 1 5 10

 <210> 108
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> mutant CDR3 region of an antibody heavychain
 variable region

 <400> 108
 Ala Lys His Thr Gly Arg Gly Val Trp Asp Pro Ile Asp Tyr
 1 5 10

 <210> 109
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> mutant CDR3 region of an antibody heavychain
 variable region

 <400> 109
 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Tyr Tyr
 1 5 10

 <210> 110
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> VH1C Back eukaryotic primer

<400> 110
 ggactagtcc tggagtgcgc gcactcccag gtccagctgg tgcagtctgg gggaggcttg 60
 gtacag 66

<210> 111
 <211> 73
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VKexpress-MUC-for primer

<400> 111
 gcgctcgcat ttgcctgtta attaagttag atctattcta ctcacgtttg atatccactt 60
 tgggtcccagg gcc 73

<210> 112
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MUC1-VL-Back-APA primer

<400> 112
 ccagtgcact ccgaaattgt gctgactcag tctcc 35

<210> 113
 <211> 296
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(294)

<400> 113
 gag gtg cag ctg ttg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agc agc tat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc 144
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca gct att agt ggt agt ggt ggt agc aca tac tac gca gac tcc gtg 192
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta tat tac tgt 288
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 85 90 95

gcg aaa ga 296
 Ala Lys

<210> 114
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 114
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 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
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 Ala Lys

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 gag ccg gcc tcc atc tcc tgc agg tct agt cag agc ctc ctg cat agt 96
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
 20 25 30
 aat gga tac aac tat ttg gat tgg tac ctg cag aag cca ggg cag tct 144
 Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 cca cag ctc ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc cct 192
 Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
 50 55 60

gac agg ttc agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc 240
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80

agc aga gtg gag gct gag gat gtt ggg gtt tat tac tgc atg caa gct 288
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95

cta caa act cct cct 303
 Leu Gln Thr Pro Pro
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<213> Homo sapiens

<400> 116

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
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 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
 20 25 30
 Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95
 Leu Gln Thr Pro Pro
 100